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OM protein - protein search, using sw model

Run on: April 25, 2005, 15:47:42 ; Search time 168 Seconds
(without alignments)
43.741 Million cell updates/sec

Title: US-10-758-572-1

Perfect score: 122

Sequence: 1 GYWSWIRQPRGKEWIG 19

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A.GeneSeq.16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122	100.0	19	5	Aae27949 Human 16/
2	122	100.0	19	8	Adq91214 Human com
3	122	100.0	19	8	Adt14722 Synthetic
4	122	100.0	20	5	Aae27961 Human 16/
5	119	97.5	19	5	Aae27958 Human 16/
6	117	95.9	19	5	Aae27956 Human 16/
7	116	95.1	252	5	Abp45315 Human Bly
8	115	95.1	252	7	Adg96142 Single ch
9	115	94.3	119	2	Aar54799 SPA-react
10	114	93.4	19	5	Aae27959 Human 16/
11	114	93.4	19	5	Aae27960 Human 16/
12	114	93.4	19	5	Aae27955 Human 16/
13	114	93.4	80	2	Aaw62794 Amino aci
14	114	93.4	97	2	Aay05694 Multiple
15	114	93.4	97	5	Abg78213 Human Fv
16	114	93.4	97	5	Abg78211 Human Fv
17	114	93.4	97	5	Abg78212 Human Fv
18	114	93.4	97	5	Abg91904 Human ant
19	114	93.4	97	5	Abg91902 Human ant
20	114	93.4	97	5	Abg91903 Human ant
21	114	93.4	97	6	Abc27107 Human ger
22	114	93.4	97	6	Abc27117 Human ger
23	114	93.4	97	6	Abc27116 Human ger
24	114	93.4	97	7	Abd75646 Human pro
25	114	93.4	97	7	Add28104 Lymphoma

26	114	93.4	97	7	Add28114 Lymphoma
27	114	93.4	97	7	Add28120 Lymphoma
28	114	93.4	97	7	Add28117 Lymphoma
29	114	93.4	97	7	Adf10048 VEGF anti
30	114	93.4	97	7	Adf10150 Antibody
31	114	93.4	97	7	Adf09942 Antibody
32	114	93.4	97	7	Adf80323 VH gene 1
33	114	93.4	98	7	Adf76908 Anti-IGF-
34	114	93.4	99	7	AAy42967 BAA75036-
35	114	93.4	102	7	Adf32174 Human int
36	114	93.4	107	2	Aar12267 Anti-huma
37	114	93.4	114	3	AAB01949 Anti-Id1
38	114	93.4	114	3	AAB01950 Anti-Id1
39	114	93.4	114	3	AAB01953 Anti-Id1
40	114	93.4	114	3	AAB01959 High affi
41	114	93.4	114	3	AAB01952 Anti-Id1
42	114	93.4	114	3	AAB01955 Streptati
43	114	93.4	114	3	AAB01951 Anti-Id1
44	114	93.4	114	3	AAB01948 Wild-type
45	114	93.4	114	3	AAB01954 Anti-Id1

ALIGNMENTS.

RESULT 1
ID AAE27949 standard; peptide; 19 AA.
XX AAE27949;

XX 27-DEC-2002 (first entry)

DE Human 16/61d mab VH chain CDRI peptide, hCDRI.

XX Complementarity-determining region; CDR; variable heavy chain; VH; VL;

KW variable light chain; SLR-associated response; immunosuppressive; SLR;

KW systemic lupus erythematosus; dermatological; therapy; anti-inflammatory;

human.

XX Homo sapiens.

OS WO200267848-A2.

XX 06-SEP-2002.

XX 26-FEB-2002; 2002WO-IL000148.

XX 26-FEB-2001; 2001IL-00141647.

XX (YEDA) YEDA RES & DEV CO LTD.

XX Mozes E;

XX WPI; 2002-698624/75.

XX New synthetic peptide useful for treating and ameliorating the clinical

XX manifestations of systemic lupus erythematosus (SLE) by modulating SLE-

XX associated responses.

XX Claim 9; Page 6; 120pp; English.

XX The invention relates to a synthetic peptide selected from a peptide of

XX 12-30 amino acid residues with a sequence of, or found within, a

XX complementarity-determining region (CDR) on the variable heavy (VH) or

XX light (VL) chain of human monoclonal anti-DNA 16/61d antibody (hCDR). The

XX composition comprising the peptide is useful for the treatment of

XX systemic lupus erythematosus (SLE) and amelioration of the clinical

XX manifestations of the disease, particularly by modulating SLE-associated

XX responses. The present sequence is human 16/61d mab VH chain CDR peptide

XX Sequence 19 AA;

AC AAE27961;

DT	27-DEC-2002	(first entry)
XX		
DE	Human 16/61d mAb VH chain CDR1 peptide mutant #1.	
XX		
KW	Complementarity-determining region; CDR; variable heavy chain; VH; VL;	
RK	variable light chain; SLE-associated response; immunosuppressive; SLE;	
KM	systemic lupus erythematosus; dermatological; therapy; antiinflammatory;	
human.		
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
FN	MO200267848-A2.	
XX		
PD	06-SEP-2002.	
XX		
XX	26-FEB-2002; 2002WO-IL000148.	
PF		
XX		
PR	26-FEB-2001; 2001IL-00141647.	
XX		
PA	(YEDA) YEDA RES & DEV CO LTD.	
XX		
P1	Mozes E;	
XX		
DR	WPI; 2002-698624/75.	
PT		
PT	New synthetic peptide useful for treating and ameliorating the clinical	
PT	manifestations of systemic lupus erythematosus (SLE) by modulating SLE-	
XX	associated responses.	
PS		
Claim 8; Page 15; 120pp; English.		
XX		
CC	The invention relates to a synthetic peptide selected from a peptide of	
CC	12-30 amino acid residues with a sequence of, or found within, a	
CC	complementarity-determining region (CDR) on the variable heavy (VH) or	
CC	light (VL) chain of human monoclonal anti-DNA 16/61d antibody (hCDR). The	
CC	composition comprising the peptide is useful for the treatment of	
CC	systemic lupus erythematosus (SLE) and amelioration of the clinical	
CC	manifestations of the disease, particularly by modulating SLE-associated	
CC	responses. The present sequence is a mutant created by addition of Thr	
XX	residue to the N-terminus of human 16/61d mAb VH chain CDR peptide	
Sequence 20 AA:		
Query Match	100.0%; Score 122; DB 5; Length 20;	
Best Local Similarity	100.0%; Pred. No. 8.1e-08;	
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0,		
OY	1 GYWSWIRQPPGKGGEWIG 19	
Db	2 GYWSWIRQPPGKGGEWIG 20	
RESULT 5		
AAB27958		
ID	AAB27958 standard; peptide; 19 AA.	
XX		
AC	AAB27958;	
XX		
DT	27-DEC-2002 (first entry)	
XX		
DE	Human 16/61d mAb VH chain CDR1 peptide mutant, R8X.	
XX		
KW	Complementarity-determining region; CDR; variable heavy chain; VH; VL;	
KM	variable light chain; SLE-associated response; immunosuppressive; SLE;	
KM	systemic lupus erythematosus; dermatological; therapy; antiinflammatory;	
human.		
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
Key	Location/Qualifiers	
TH	Misc-difference 8	
LT		

FT		/note= "Wild-type Arg is replaced with Lys"
XX		
XX	WO200267848-A2.	
PN		
PD	06-SEP-2002.	
XX		
XX	26-FEB-2002; 2002WO-IL000148.	
PE		
XX	26-FEB-2001; 2001IL-00141647.	
PR		
XX		
XX	(YEDA) YEDA RES & DEV CO LTD.	
PA		
PI	Mozes E;	
DR	WPI; 2002-698624/75.	
XX		
XX	New synthetic peptide useful for treating and ameliorating the clinical	
PT	manifestations of systemic lupus erythematosus (SLE) by modulating SLE-	
PT	associated responses.	
XX		
XX	Claim 8; Page 15; 120pp; English.	
PS		
XX		
CC	The invention relates to a synthetic peptide selected from a peptide of	
CC	12-30 amino acid residues with a sequence of, or found within, a	
CC	complementarity-determining region (CDR) on the variable heavy (VH) or	
CC	light (VL) chain of human monoclonal anti-DNA 16/61d antibody (hCDR). The	
CC	composition comprising the peptide is useful for the treatment of	
CC	systemic lupus erythematosus (SLE) and amelioration of the clinical	
CC	manifestations of the disease, particularly by modulating SLE-associated	
CC	responses. The present sequence is human 16/61d mAb VH chain CDR mutant	
CC	peptide	
XX		
XX	Sequence 19 AA;	
SQ		
	Query Match	97.5%; Score 119; DB 5; Length 19;
	Best Local Similarity	94.7%; Pred. No. 1.8e-07;
	Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 GYWSWIRPPGKGGEWIG 19	
	:	
	1 GYWSWIKPPGKGGEWIG 19	
DB		
	RESULT 6	
	AAE27956	
ID	AAE27956 standard; peptide; 19 AA.	
XX		
XX	AAE27956;	
AC		
XX		
DT	27-DEC-2002 (first entry)	
XX		
DE	Human 16/61d mAb VH chain CDR1 peptide mutant, E15S.	
XX		
KM	Complementarity-determining region; CDR; variable heavy chain; VH; VL;	
KM	variable light chain; SLR-associated response; immunosuppressive; SLR;	
KM	systemic lupus erythematosus; dermatological; therapy; antiinflammatory;	
human.		
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
XX	Key	Location/Qualifiers
FT	Misc-difference 15	
FT	/note= "Wild-type Glu is replaced with Ser"	
XX		
XX	WO200267848-A2.	
PN		
XX		
XX	06-SEP-2002.	
PD		
XX		
PF	26-FEB-2002; 2002WO-IL000148.	
XX		
XX	26-FEB-2001; 2001IL-00141647.	
PR		
XX		

PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Mozes E;
 XX
 DR WPI; 2002-698624/75.
 XX
 PT New synthetic peptide useful for treating and ameliorating the clinical
 PT manifestations of systemic lupus erythematosus (SLE) by modulating SLE-
 PT associated responses.
 XX
 PS Claim 8; Page 15; 120pp; English.
 XX
 CC The invention relates to a synthetic peptide selected from a peptide of
 CC 12-30 amino acid residues with a sequence of, or found within, a
 CC complementarity-determining region (CDR) on the variable heavy (VH) or
 CC light (VL) chain of human monoclonal anti-DNA 16/61d antibody (hCDR). The
 CC composition comprising the peptide is useful for the treatment of
 CC systemic lupus erythematosus (SLE) and amelioration of the clinical
 CC manifestations of the disease, particularly by modulating SLE-associated
 CC responses. The present sequence is human 16/61d mAb VH chain CDR mutant
 CC peptide
 CC
 SQ Sequence 19 AA;
 XX
 XX
 Query Match 95.9%; Score 117; DB 5; Length 19;
 Best Local Similarity 94.7%; Pred. No. 3.1e-07;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 GYYSWIRPPGKGEWIG 19
 DB 1 GYYSWIRPPGKGEWIG 19
 XX
 XX
 RESULT 7
 ABP45315
 ID ABP45315 standard; protein; 252 AA.
 XX
 AC ABP45315;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human BlyS binding scFv SEQ ID 1326.
 XX
 KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antithematic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO200202641-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US019110.
 XX
 PR 16-JUN-2000; 2000US-0212210P.
 PR 17-OCT-2000; 2000US-0240816P.
 PR 16-MAR-2001; 2001US-0276248P.
 PR 21-MAR-2001; 2001US-0277379P.
 PR 25-MAY-2001; 2001US-0293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX
 DR WPI; 2002-114799/15.
 XX
 PT Antibodies against B lymphocyte stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.

XX
 PS Claim 1; Page 1985-1986; 3148pp; English.
 XX
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (BlyS) polypeptides. BlyS is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antithematic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS
 CC and so may be used to detect and quantitate the presence of BlyS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BlyS. They may also be
 CC administered to treat diseases associated with aberrant BlyS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 CC
 SQ Sequence 252 AA;
 XX
 XX
 Query Match 95.1%; Score 116; DB 5; Length 252;
 Best Local Similarity 94.7%; Pred. No. 4.9e-06;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 GYYSWIRPPGKGEWIG 19
 DB 31 GYYSWIRPPGKGEWIG 49
 XX
 XX
 RESULT 8
 ADG96142
 ID ADG96142 standard; protein; 252 AA.
 XX
 AC ADG96142;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Single chain antibody that immunospecifically binds BlyS SeqID 1326.
 XX
 KW antibody; B lymphocyte stimulator; BlyS; tumour necrosis factor;
 KW B cell proliferation; differentiation; scFv; myasthenia gravis;
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
 KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
 KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.
 XX
 OS Unidentified.
 XX
 PN WO2003055979-A2.
 XX
 PD 10-JUL-2003.
 XX
 PF 14-NOV-2002; 2002WO-US036496.
 XX
 PR 16-NOV-2001; 2001US-0331469P.
 PR 19-DEC-2001; 2001US-0340817P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Barash SC, Choi GH, Vaughan TV, Hilbert D;
 XX
 DR WPI; 2003-505530/47.
 XX
 PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
 PT (BlyS), useful for detecting and treating diseases or disorders e.g.
 PT rheumatoid arthritis, asthma and leukemia.
 XX
 PS Example 1; SEQ ID NO 1326; 394pp; English.
 XX
 CC This invention relates to novel antibodies that immunospecifically bind
 CC to B lymphocyte stimulator (BlyS). The BlyS gene has been mapped to

CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antirheumatic, antiarthritis, neuroprotective,
CC antiinflammatory, antiallergic, antitumor and cytostatic. This
CC polypeptide sequence is a single chain antibody that binds Blys of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 252 AA;

Query Match 95.1%; Score 116; DB 7; Length 252;
Best Local Similarity 94.7%; Pred. No. 4.9e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRQPPKGEWIG 19
|||
Db 31 GYWSWIRQPPKGEWIG 49

RESULT 9
AAR54799
ID AAR54799 standard; peptide; 119 AA.
XX
XX AAR54799;
AC
XX 25-MAR-2003 (revised)
DT 18-OCT-1994 (first entry)
XX
XX SPA-reactive Igm heavy chain clone LES.
DE
XX
KM SPA domain D; Ig binding region; Igm; B-cell superantigen; sAg;
KM superantigen; heavy chain variable region; VH3 restricted antibody; VH;
KM protein-A; LES; B-lymphocyte; vaccine.
XX
XX Homo sapiens.
OS
XX
XX W09409818-A1.
PN
XX 11-MAY-1994.
PD
XX 29-OCT-1993; 93WO-US010555.
PF
XX 30-OCT-1992; 92US-00969936.
PR
XX
XX (REGC) UNIV CALIFORNIA.
PA
XX
XX Silverman GJ;
PI
XX
XX WPI; 1994-167127/20.
DR
XX
XX Stimulating prodn. of variable region gene family restricted antibodies -
PT through B-cell super-antigen vaccination.
XX
XX
XX PS Disclosure; Page 81; 130pp; English.

CC A B-cell superantigen (sAg) is a fragment of SPA D domain that
CC specifically binds the Fab portion of variable region restricted
CC antibodies. The sAg is used to enhance production of VH, especially VH3,
CC restricted Abs. During attempts to identify sAgs, aa sequences (AAR54784-
CC 801) of H chains from Ig reactive with mod-SPA, and aa and DNA sequences

CC (AAR54802-16, AAO64842-56) of VH regions of SPA binders obtained from
CC combinatorial libraries were determined. (Updated on 25-MAR-2003 to
CC correct FN field.)
XX
XX Sequence 119 AA;

QY 1 GYWSWIRQPPKGEWIG 19
|||
Db 31 GYWSWIRQPPKGEWIG 49

RESULT 10
AAE27959
ID AAE27959 standard; peptide; 19 AA.
XX
XX AAE27959;
AC
XX 27-DEC-2002 (first entry)
DT
XX
XX Human 16/61d mAb VH chain CDR1 peptide mutant, P10S.
DE
XX
KM Complementarity-determining region; CDR; variable heavy chain; VH; VL;
KM variable light chain; SLE-associated response; immunosuppressive; SLE;
KM systemic lupus erythematosus; dermatological; therapy; antiinflammatory;
KM human.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX Key Location/Qualifiers
FH
FT .Misc-difference 10 /note= "Wild-type Pro is replaced with Ser"
FT
XX
XX W0200267848-A2.
FN
XX
XX 06-SEP-2002.
PD
XX
XX 26-FEB-2002; 2002WO-IL000148.
PF
XX
XX 26-FEB-2001; 2001IL-00141647.
PR
XX
XX (YEDA) YEDA RES & DEV CO LTD.
PA
XX
XX Mozes E;
PI
XX
XX WPI; 2002-698624/75.
DR
XX
XX
XX New synthetic peptide useful for treating and ameliorating the clinical
PT manifestations of systemic lupus erythematosus (SLE) by modulating SLE-
PT associated responses.
XX
XX
XX Claim 8; Page 15; 120pp; English.
PS
XX
XX The invention relates to a synthetic peptide selected from a peptide of
CC 12-30 amino acid residues with a sequence of, or found within, a
CC complementarity-determining region (CDR) on the variable heavy (VH) or
CC light (VL) chain of human monoclonal anti-DNA 16/61d antibody (hCDR). The
CC composition comprising the peptide is useful for the treatment of
CC systemic lupus erythematosus (SLE) and amelioration of the clinical
CC manifestations of the disease, particularly by modulating SLE-associated
CC responses. The present sequence is human 16/61d mAb VH chain CDR mutant
CC peptide
XX
XX
XX Sequence 19 AA;

Query Match 93.4%; Score 114; DB 5; Length 19;
Best Local Similarity 94.7%; Pred. No. 7e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19
 |||||
 DB 1 GYWSWIRPPGKGEWIG 19

RESULT 11
 AAE27960
 ID AAE27960 standard; peptide; 19 AA.
 XX
 AC AAE27960;
 XX
 DT 27-DEC-2002 (first entry)
 XX
 DE Human 16/61d mAb VH chain CDR1 peptide mutant, G12E.
 XX
 KM Complementarity-determining region; CDR, variable heavy chain; VH; VL;
 KM variable light chain; SLE-associated response; immunosuppressive; SLE;
 KM systemic lupus erythematosus; dermatological; therapy; antiinflammatory;
 KM human.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 12 /note= "Wild-type Gly is replaced with Glu"
 FT
 FN WO200267848-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 26-FEB-2002; 2002WO-IL000148.
 XX
 PR 26-FEB-2001; 2001IL-00141647.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Mozes E;
 XX
 DR WPI; 2002-698624/75.
 XX
 PT New synthetic peptide useful for treating and ameliorating the clinical
 PT manifestations of systemic lupus erythematosus (SLE) by modulating SLE-
 associated responses.
 XX
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 CC The invention relates to a synthetic peptide selected from a peptide of
 CC 12-30 amino acid residues with a sequence of, or found within, a
 CC complementarity-determining region (CDR) on the variable heavy (VH) or
 CC light (VL) chain of human monoclonal anti-DNA 16/61d antibody (hCDR). The
 CC composition comprising the peptide is useful for the treatment of
 CC systemic lupus erythematosus (SLE) and amelioration of the clinical
 CC manifestations of the disease, particularly by modulating SLE-associated
 CC responses. The present sequence is human 16/61d mAb VH chain CDR mutant
 CC peptide
 CC
 SQ Sequence 19 AA;
 QY
 DB 1 GYWSWIRPPGKGEWIG 19
 |||||
 1 GYWSWIRPPGKGEWIG 19

Query Match 93.4%; Score 114; DB 5; Length 19;
 Best Local Similarity 94.7%; Pred. No. 7e-07; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 12
 AAE27955
 ID AAE27955 standard; peptide; 19 AA.
 XX
 AC AAE27955;

XX
 DT 27-DEC-2002 (first entry)
 XX
 DE Human 16/61d mAb VH chain CDR1 peptide mutant, E15L.
 XX
 KM Complementarity-determining region; CDR, variable heavy chain; VH; VL;
 KM variable light chain; SLE-associated response; immunosuppressive; SLE;
 KM systemic lupus erythematosus; dermatological; therapy; antiinflammatory;
 KM human.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 15 /note= "Wild-type Glu is replaced with Leu"
 FT
 FN WO200267848-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 26-FEB-2002; 2002WO-IL000148.
 XX
 PR 26-FEB-2001; 2001IL-00141647.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Mozes E;
 XX
 DR WPI; 2002-698624/75.
 XX
 PT New synthetic peptide useful for treating and ameliorating the clinical
 PT manifestations of systemic lupus erythematosus (SLE) by modulating SLE-
 associated responses.
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 PS Claim 8; Page 15; 120pp; English.
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 CC complementarity-determining region (CDR) on the variable heavy (VH) or
 CC light (VL) chain of human monoclonal anti-DNA 16/61d antibody (hCDR). The
 CC composition comprising the peptide is useful for the treatment of
 CC systemic lupus erythematosus (SLE) and amelioration of the clinical
 CC manifestations of the disease, particularly by modulating SLE-associated
 CC responses. The present sequence is human 16/61d mAb VH chain CDR mutant
 CC peptide
 CC
 SQ Sequence 19 AA;
 QY
 DB 1 GYWSWIRPPGKGEWIG 19
 |||||
 1 GYWSWIRPPGKGEWIG 19

Query Match 93.4%; Score 114; DB 5; Length 19;
 Best Local Similarity 94.7%; Pred. No. 7e-07; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 13
 AAM62794
 ID AAM62794 standard; peptide; 80 AA.
 XX
 AC AAM62794;
 XX
 DT 23-SEP-1998 (first entry)
 XX
 DE Amino acid sequence of a human antibody fragment.
 XX
 KM Human; immunoglobulin; Ig; transgenic; non-human mammal;
 KM inactivated endogenous Ig locus; B-cell development;
 KM human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;
 KM kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;
 KM production; antibody.

XX Homo sapiens.
 OS WO9824893-A2.
 PN 11-JUN-1998.
 PD
 XX
 PF 03-DEC-1997; 97WO-US023091.
 XX
 PR 03-DEC-1996; 96US-00759620.
 XX
 PA (ABGE-) ABGENIX INC.
 XX
 PI Jakobovics A, Kucheraipacti R, Klapholz S, Nendez M, Green L;
 XX WPI; 1998-333314/29.
 DR
 XX
 PT New transgenic non-human mammals - having an inactivated immunoglobulin
 PT locus and a near complete human immunoglobulin locus, used for production
 PT of human antibodies.
 XX
 XX Disclosure; Page 71; 128pp; English.
 PS
 XX
 CC AAM62793-822 represent fragments of human antibodies produced by
 CC transgenic Xenomice, created using the method of the invention. The
 CC specification describes a transgenic non-human mammal which has genome
 CC modifications that comprise an inactivated endogenous immunoglobulin (Ig)
 CC locus, so that the mammal does not display normal B-cell development. The
 CC modified genome also has an inserted human heavy chain Ig locus in
 CC germline configuration, the human heavy chain Ig locus comprising a human
 CC micro constant region and regulatory and switch sequences, human J-H
 CC genes, human D-H genes, and human V-H genes and an inserted human kappa
 CC light chain Ig locus in germline configuration, the human kappa light
 CC chain Ig locus comprising a human kappa constant region, J-kappa genes,
 CC and V-kappa genes, where the number of V-H and V-kappa genes inserted are
 CC selected to restore normal B-cell development in the mammal. The
 CC transgenic animals have a near complete human Ig locus, including both a
 CC human heavy chain locus and a human kappa light chain locus. They can be
 CC used for the production of human antibodies when exposed to particular
 CC antigens e.g. when exposed to human IL-8, EGFR or TNF- alpha the mice
 CC will produce antibodies to IL-8, EGFR or TNF- alpha respectively
 XX
 SO Sequence 80 AA;
 Query Match 93.4%; Score 114; DB 2; Length 80;
 Best Local Similarity 94.7%; Pred. No. 2.8e-06;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GYWSMTROPKGEWIG 19
 |||||
 14 GYWSMTROPKGEWIG 32
 DB
 RESULT 14
 AAY05694
 ID AAY05694 standard; protein, 97 AA.
 XX
 AC AAY05694;
 XX
 DT 19-JUN-1999 (first entry)
 XX
 DE Multiple sclerosis patient CSF B-cell VH region (clone 4d76).
 XX
 KM Multiple sclerosis; cerebrospinal fluid; CSF; B-cell;
 KM heavy chain variable region; VH gene; somatic hypermutation;
 XX B-cell clonality; RA gene; diagnosis; human.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Region 1..30
 FT /label= FR1
 FT Misc-difference 8

FT /note= "encoded by GGC"
 FT Misc-difference 13
 FT /note= "replaces Glu of RA"
 FT Misc-difference 14
 FT /note= "encoded by CCT"
 FT Misc-difference 23
 FT /note= "replaces Gly of RA"
 FT Misc-difference 25
 FT /note= "replaces Phe of RA"
 FT Misc-difference 30
 FT /note= "replaces Gly of RA"
 FT Region 31..36
 FT /label= CDR1
 FT Misc-difference 31
 FT /note= "replaces Gly of RA"
 FT Misc-difference 32
 FT /note= "replaces Phe of RA"
 FT Region 37..50
 FT /label= FR2
 FT Region 51..66
 FT /label= CDR2
 FT Misc-difference 56
 FT /note= "replaces Asn of RA"
 FT Misc-difference 57
 FT /note= "replaces Ser of RA"
 FT Misc-difference 58
 FT /note= "replaces Lys of RA"
 FT Region 67..97
 FT /label= FR3
 FT Misc-difference 71
 FT /note= "replaces Leu of RA"
 FT Misc-difference 81
 FT /note= "replaces Arg of RA"
 FT
 FT WO9915696-A1.
 PN 01-APR-1999.
 PD
 XX
 XX 17-SEP-1998; 98WO-CA000873.
 PF
 XX 19-SEP-1997; 97CA-02216595.
 PR 04-NOV-1997; 97CA-02220245..
 XX
 XX (QINV/) QIN Y.
 PA
 XX
 XX QIN Y;
 PI
 XX WPI; 1999-276985/23.
 DR N-PSDB; AAX25318.
 XX
 DT Determination of B-cell clonality by amplification or enzymatic
 DT digestion.
 FT
 FT
 XX
 PS Disclosure; Fig 9D; 67pp; English.
 XX
 CC This sequence represents a heavy chain variable region (VH) as predicted
 CC from DNA of dominant clone 4d76 of B-cells taken from the cerebrospinal
 CC fluid (CSF) of a multiple sclerosis (MS) patient. Sequences of VH of CSF
 CC B-cells were obtained from 4 MS patients (see AAX25316-19). Differences
 CC in nucleotide and predicted amino acid (see AAY05691-94) sequences were
 CC compared with the closest known germline VH genes, for 4d76, this was RA.
 CC The results provided direct evidence that intrathecal clonally expanded B
 CC -cells from the CSF of MS patients are hypermutated postgerminal centre
 CC antibody-forming or memory lymphocytes that have undergone antigen
 CC selection. This finding implicates an important pathogenic pathway for
 CC the development of demyelination in CNS of MS. The invention provides
 CC assay kits for determining B-cell or T-cell clonality. This technology
 CC allows the establishment of clonal, specific RNA library from pathogenic
 CC cells in the CNS of patients, which is important for further
 CC understanding of the role of antigen(s) in the cause of B-cell clonal
 CC expansion, and towards developing antigen specific therapeutic strategy
 XX
 SO Sequence 97 AA;

Search completed: April 25, 2005, 16:02:48
Job time : 170 secs

Query Match 93.4%; Score 114; DB 2; Length 97;
Best Local Similarity 94.7%; Pred. No. 3.4e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYWSWIRPPGKGEWIG 19
| | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |
Db 31 GYWSWIRPPGKGEWIG 49

RESULT 15

ABG78213
ID ABG78213 standard; protein; 97 AA.

XX ABG78213;

XX 15-NOV-2002 (first entry)

XX Human Fv molecule hypervariable region related peptide #88.

XX Human; Fv molecule; hypervariable region; single chain Fv; cytosolic;

XX disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;

XX Lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

XX Homo sapiens.

XX NO200259264-A2.

XX 01-AUG-2002.

XX 31-DEC-2001; 2001MO-US049440.

XX 29-DEC-2000; 2000US-00751181.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;

XX Plaksin D, Peretz T;

XX WPI; 2002-619166/66.

XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct

XX PT fragment, or construct of fragment with enhanced binding

XX PT characteristics so as to selectively bind target cell in favor of other

XX cells.

XX Claim 13; Page 193-194; 232pp; English.

XX The invention relates to a peptide or polypeptide comprising an Fv

XX molecule, a construct or fragments which selectively and/or specifically

XX enhanced binding characteristics which selectively and/or specifically

XX binds to a target cell in favour of other cells, where binding is

XX primarily determined by a first hypervariable region and Fv is a single

XX chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in

XX association with or attached, coupled, combined, linked or fused to a

XX pharmaceutical agent, is useful in the manufacture of a medicament, where

XX the medicament has activity against a diseased cell, preferably a cancer

XX cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,

XX myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an

XX acute myeloid leukaemia cell). The peptide is also useful for preparing a

XX composition for use in inhibiting the growth of a diseased or cancer

XX cell. This sequence represents a human Fv molecule hypervariable region

XX related peptide of the invention

XX SQ Sequence 97 AA;

Qy 1 GYWSWIRPPGKGEWIG 19
| | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |
Db 31 GYWSWIRPPGKGEWIG 49

Query Match 93.4%; Score 114; DB 5; Length 97;
Best Local Similarity 94.7%; Pred. No. 3.4e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: April 25, 2005, 16:00:09 ; Search time 42 Seconds
(without alignments)
33.770 Million cell updates/sec

Title: US-10-758-572-1

Perfect score: 122
Sequence: 1 GYWSWIRQPGKGEWIG 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 7464964 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
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6: /cgn2_6/ptodata/1/aa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	115	94.3	119	2	US-08-428-197-16
2	115	94.3	119	5	PCT-US93-10555-16
3	114	93.4	116	3	US-08-545-809A-118
4	114	93.4	123	3	US-08-793-450-4
5	114	93.4	139	4	US-09-203-768A-2
6	114	93.4	472	3	US-08-793-450-8
7	114	93.4	473	4	US-09-049-672A-4
8	110	90.2	117	4	US-09-720-493-2
9	110	90.2	124	1	US-08-476-039-78
10	110	90.2	124	1	US-08-476-349A-78
11	108	88.5	76	3	US-08-851-362D-22
12	108	88.5	96	3	US-08-851-362D-35
13	108	88.5	97	3	US-08-851-362D-33
14	108	88.5	98	1	US-08-476-039-75
15	108	88.5	98	1	US-08-476-349A-75
16	108	88.5	116	3	US-08-545-809A-140
17	108	88.5	117	3	US-08-851-362D-48
18	108	88.5	117	4	US-09-232-290-47
19	108	88.5	118	3	US-08-545-809A-142
20	108	88.5	118	3	US-08-851-362D-47
21	108	88.5	118	3	US-09-025-769B-25
22	108	88.5	118	4	US-09-490-070A-25
23	108	88.5	118	4	US-09-490-153-25
24	108	88.5	118	4	US-09-490-324-25
25	108	88.5	119	2	US-08-652-816A-10
26	108	88.5	119	3	US-09-025-769B-39
27	108	88.5	119	3	US-09-025-769B-65

28	108	88.5	119	4	US-09-490-070A-39	Sequence 39, Appl
29	108	88.5	119	4	US-09-490-070A-65	Sequence 65, Appl
30	108	88.5	119	4	US-09-490-153-39	Sequence 39, Appl
31	108	88.5	119	4	US-09-490-153-65	Sequence 65, Appl
32	108	88.5	119	4	US-09-490-324-39	Sequence 39, Appl
33	108	88.5	119	4	US-09-490-324-65	Sequence 65, Appl
34	108	88.5	120	4	US-09-424-840B-20	Sequence 20, Appl
35	108	88.5	139	4	US-09-471-276-837	Sequence 837, App
36	108	88.5	219	3	US-09-460-384-37	Sequence 37, Appl
37	108	88.5	244	3	US-08-918-148-79	Sequence 79, Appl
38	108	88.5	244	4	US-09-138-091A-77	Sequence 77, Appl
39	106	86.9	140	4	US-09-471-276-850	Sequence 850, App
40	105	86.1	76	3	US-08-851-362D-19	Sequence 19, Appl
41	105	86.1	76	4	US-09-472-087-85	Sequence 85, Appl
42	105	86.1	118	3	US-08-545-809A-116	Sequence 116, App
43	105	86.1	150	4	US-09-582-337-14	Sequence 14, Appl
44	104	85.2	111	4	US-09-471-276-840	Sequence 840, App
45	104	85.2	118	3	US-08-545-809A-123	Sequence 123, App

ALIGNMENTS

RESULT 1
US-08-428-197-16
Sequence 16, Application US/08428197
Patent No. 5691438
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,197
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-2630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5110
TELEFAX: (619) 455-5110
INFORMATION FOR SEO ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: LBS
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..119
US-08-428-197-16

Query Match 94.3%; Score 115; DB 2; Length 119;
Best Local Similarity 89.5%; Pred. No. 8.3e-08;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19
|||||:|||||
Db 31 GYWSWIRPPGKGEWIG 49

RESULT 2
PCT-US93-10555-16

; Sequence 16, Application PC/TUS9310555
; GENERAL INFORMATION:

; APPLICANT: SILVERMAN, GREGG J.
; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
; TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East - Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10555
; FILING DATE: 29-OCT-1993

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: PD-2630

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 119 amino acids
; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:

; CLONE: LBS

; FEATURE:

; NAME/KEY: Peptide
; LOCATION: 1..119

; PCT-US93-10555-16

Query Match 94.3%; Score 115; DB 5; Length 119;
Best Local Similarity 89.5%; Pred. No. 8.3e-08;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19
|||||:|||||
Db 31 GYWSWIRPPGKGEWIG 49

RESULT 3

US-08-545-809A-118

; Sequence 118, Application US/08545809A
; Patent No. 6096878

; GENERAL INFORMATION:

; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko

; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows95

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 118:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 116 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein

; US-08-545-809A-118

Query Match 93.4%; Score 114; DB 3; Length 116;
Best Local Similarity 94.7%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19
|||||:|||||
Db 50 GYWSWIRPPGKGEWIG 68

RESULT 4

US-08-793-450-4

; Sequence 4, Application US/08793450
; Patent No. 6312690

; GENERAL INFORMATION:

; APPLICANT: EDELMAN, LENA
; APPLICANT: MARGARITTE, CHRISTEL

; APPLICANT: KACZOREK, MICHEL
; APPLICANT: CHABIBI, HASSAN

; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHSUS D

; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/793,450

FILING DATE: 03-MAR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-793-450-4

Query Match 93.4%; Score 114; DB 3; Length 123;
Best Local Similarity 94.7%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GYWSWIRPPGKGEWIG 19
Db 31 GYWSWIRPPGKGEWIG 49

RESULT 5
US-09-203-768A-2
Sequence 2, Application US/09203768A
Patent No. 6787638
GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Watkins, Jeffrey D.
TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods
TITLE OF INVENTION: of use
FILE REFERENCE: P-IX 2947
CURRENT APPLICATION NUMBER: US/09/203,768A
CURRENT FILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 139
TYPE: PRT
ORGANISM: Homo sapiens
US-09-203-768A-2

Query Match 93.4%; Score 114; DB 4; Length 139;
Best Local Similarity 94.7%; Pred. No. 1.3e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GYWSWIRPPGKGEWIG 19
Db 50 GYWSWIRPPGKGEWIG 68

RESULT 6
US-08-793-450-8
Sequence 8, Application US/08793450
Patent No. 6312690
GENERAL INFORMATION:
APPLICANT: EDELMAN, LENA
APPLICANT: MARGARITTE, CHRISTEL
APPLICANT: KACZOREK, MICHEL
APPLICANT: CHABRIH, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.

STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-793-450-8

Query Match 93.4%; Score 114; DB 3; Length 472;
Best Local Similarity 94.7%; Pred. No. 4.4e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GYWSWIRPPGKGEWIG 19
Db 50 GYWSWIRPPGKGEWIG 68

RESULT 7
US-09-049-672A-4
Sequence 4, Application US/09049672A
Patent No. 6135941
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HERewith
CLASSIFICATION: 536
PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ceirone, Michael C
; REGISTRATION/DOCKET NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
;
;
;
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 473 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PANTCTUT01
; CLONE: 1513264
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US-09-049-672A-4
;
Query Match          93.4%; Score 114; DB 3; Length 473;
Best Local Similarity 94.7%; Pred. No. 4.5e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYYWSWIRPPGKGLEWIG 19
Db      52 GYYWSWIRPPGKGLEWIG 70

RESULT 8
US-09-720-493-2
; Sequence 2, Application US/09720493
; Patent No. 6827925
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Williams, Andrew J
; APPLICANT: Tempest, Philip R
; APPLICANT: Hollet, Thor L
; APPLICANT: Main, Sarah H
; APPLICANT: Jackson, Helen
; APPLICANT: Daromola, Olalekan
; TITLE OF INVENTION: Improvements relating to antibodies
; FILE REFERENCE: AHB/CP575333
; CURRENT APPLICATION NUMBER: US/09/720,493
; CURRENT FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: GB 9814383.7
; PRIOR FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-720-493-2
;
Query Match          90.2%; Score 110; DB 4; Length 117;
Best Local Similarity 89.5%; Pred. No. 3.6e-07;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GYYWSWIRPPGKGLEWIG 19
Db      32 GYYWSWIRPPGKGLEWIG 50

RESULT 9
US-08-478-039-78
; Sequence 78, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; APPLICANT: Raab, Ronald W.
```

```

; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teakin Esq., Robin L.
; REGISTRATION NUMBER: 35,010
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VH4 clone 4-16
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US-08-478-039-78
;
Query Match          90.2%; Score 110; DB 1; Length 124;
Best Local Similarity 89.5%; Pred. No. 3.8e-07;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GYYWSWIRPPGKGLEWIG 19
Db      33 GYYWSWIRPPGKGLEWIG 51

RESULT 10
US-08-476-349A-78
; Sequence 78, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
```

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STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: VH4 clone 4-16
US-08-476-349A-78

Query Match          90.2%; Score 110; DB 1; Length 124;
Best Local Similarity 89.5%; Pred. No. 3.8e-07;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGLEWIG 19
Db 33 GYWSWIRPPGKGLEWIG 51

RESULT 11
US-08-851-362D-22
Sequence 22, Application US/08851362D
Patent No. 6235883
GENERAL INFORMATION:
APPLICANT: Jakobovits, Aya
APPLICANT: Yang, Xiao-Dong
APPLICANT: Gallo, Michael
APPLICANT: Jia, Xiao-Chi
TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
TITLE OF INVENTION: Growth Factor Receptor
FILE REFERENCE: Cell 4.20
CURRENT APPLICATION NUMBER: US/08/851,362D
CURRENT FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 76
TYPE: PRT
ORGANISM: human
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US-08-851-362D-22
Query Match          88.5%; Score 108; DB 3; Length 76;
Best Local Similarity 94.4%; Pred. No. 4.2e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YYWSWIRPPGKGLEWIG 19
Db 11 YYWSWIRPPGKGLEWIG 28

RESULT 12
US-08-851-362D-35
Sequence 35, Application US/08851362D
Patent No. 6235883
GENERAL INFORMATION:
APPLICANT: Jakobovits, Aya
APPLICANT: Yang, Xiao-Dong
APPLICANT: Gallo, Michael
APPLICANT: Jia, Xiao-Chi
TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
TITLE OF INVENTION: Growth Factor Receptor
FILE REFERENCE: Cell 4.20
CURRENT APPLICATION NUMBER: US/08/851,362D
CURRENT FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 35
LENGTH: 96
TYPE: PRT
ORGANISM: human
US-08-851-362D-35

Query Match          88.5%; Score 108; DB 3; Length 96;
Best Local Similarity 94.4%; Pred. No. 5.4e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YYWSWIRPPGKGLEWIG 19
Db 11 YYWSWIRPPGKGLEWIG 28

RESULT 13
US-08-851-362D-33
Sequence 33, Application US/08851362D
Patent No. 6235883
GENERAL INFORMATION:
APPLICANT: Jakobovits, Aya
APPLICANT: Yang, Xiao-Dong
APPLICANT: Gallo, Michael
APPLICANT: Jia, Xiao-Chi
TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
TITLE OF INVENTION: Growth Factor Receptor
FILE REFERENCE: Cell 4.20
CURRENT APPLICATION NUMBER: US/08/851,362D
CURRENT FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 33
LENGTH: 97
TYPE: PRT
ORGANISM: human
US-08-851-362D-33

Query Match          88.5%; Score 108; DB 3; Length 97;
Best Local Similarity 94.4%; Pred. No. 5.4e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YYWSWIRPPGKGLEWIG 19
Db 11 YYWSWIRPPGKGLEWIG 28
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RESULT 14
US-08-478-039-75
; Sequence 75: Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teekin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VH4 consensus
; US-08-478-039-75

Query Match      88.5%; Score 108; DB 1; Length 98;
Best Local Similarity 94.4%; Pred. No. 5.5e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 YVWSWIRPPGKGLEWIG 19
Db      33 YVWSWIRPPGKGLEWIG 50

RESULT 15
US-08-476-349A-75
; Sequence 75: Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
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; APPLICANT: Hanna, Nabil
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teekin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VH4 consensus
; US-08-476-349A-75

Query Match      88.5%; Score 108; DB 1; Length 98;
Best Local Similarity 94.4%; Pred. No. 5.5e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 YVWSWIRPPGKGLEWIG 19
Db      33 YVWSWIRPPGKGLEWIG 50

Search completed: April 25, 2005, 16:15:37
Job time : 43 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 16:06:05 ; Search time 134 Seconds
(without alignments)
47.187 Million cell updates/sec

Title: US-10-758-572-1

Perfect score: 122
Sequence: 1 GYWSWIRQPRGKEEWIG 19

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09C_NEW_PUB.pep.*
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- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	122	100.0	19	US-10-468-924-6 Sequence 6, Appl1
2	122	100.0	19	US-10-758-572-1 Sequence 1, Appl1
3	122	100.0	19	US-10-758-397-6 Sequence 6, Appl1
4	122	100.0	19	US-10-758-397-18 Sequence 18, Appl1
5	122	100.0	20	US-10-468-924-15 Sequence 18, Appl1
6	119	97.5	19	US-10-468-924-15 Sequence 15, Appl1
7	117	95.9	19	US-10-468-924-13 Sequence 13, Appl1
8	116	95.1	19	US-10-468-924-14 Sequence 14, Appl1
9	116	95.1	252	US-09-880-748-1326 Sequence 1326, Ap
10	116	95.1	252	US-10-293-418-1326 Sequence 1326, Ap
11	114	93.4	19	US-10-468-924-12 Sequence 12, Appl1
12	114	93.4	19	US-10-468-924-16 Sequence 16, Appl1
13	114	93.4	19	US-10-468-924-17 Sequence 17, Appl1

14	114	93.4	80	14	US-10-078-958-2	Sequence 2, Appl1
15	114	93.4	97	14	US-10-194-975-40	Sequence 40, Appl1
16	114	93.4	97	14	US-10-194-975-49	Sequence 49, Appl1
17	114	93.4	97	14	US-10-194-975-50	Sequence 50, Appl1
18	114	93.4	97	15	US-10-308-817-83	Sequence 83, Appl1
19	114	93.4	97	15	US-10-032-0378-86	Sequence 86, Appl1
20	114	93.4	97	15	US-10-032-0378-87	Sequence 87, Appl1
21	114	93.4	97	15	US-10-032-0378-88	Sequence 88, Appl1
22	114	93.4	97	15	US-10-029-988B-86	Sequence 86, Appl1
23	114	93.4	97	15	US-10-029-988B-87	Sequence 87, Appl1
24	114	93.4	97	15	US-10-029-988B-88	Sequence 88, Appl1
25	114	93.4	97	15	US-10-032-423A-86	Sequence 86, Appl1
26	114	93.4	97	15	US-10-032-423A-87	Sequence 87, Appl1
27	114	93.4	97	15	US-10-032-423A-88	Sequence 88, Appl1
28	114	93.4	97	15	US-10-453-698-83	Sequence 83, Appl1
29	114	93.4	97	15	US-10-029-926B-86	Sequence 86, Appl1
30	114	93.4	97	15	US-10-029-926B-87	Sequence 87, Appl1
31	114	93.4	97	15	US-10-029-926B-88	Sequence 88, Appl1
32	114	93.4	97	16	US-10-379-392-47	Sequence 47, Appl1
33	114	93.4	102	10	US-09-972-656-128	Sequence 128, App
34	114	93.4	114	14	US-10-027-725A-9	Sequence 9, Appl1
35	114	93.4	114	17	US-10-733-532-128	Sequence 128, App
36	114	93.4	116	14	US-10-071-866-38	Sequence 38, Appl1
37	114	93.4	116	14	US-10-071-866-38	Sequence 38, Appl1
38	114	93.4	116	15	US-10-360-828-38	Sequence 38, Appl1
39	114	93.4	116	15	US-10-338-366-6	Sequence 6, Appl1
40	114	93.4	117	15	US-10-309-762-127	Sequence 127, App
41	114	93.4	117	9	US-09-864-761-44315	Sequence 44315, A
42	114	93.4	118	15	US-10-371-942-90	Sequence 90, Appl1
43	114	93.4	118	15	US-10-388-214A-36	Sequence 36, Appl1
44	114	93.4	119	14	US-10-078-958-3	Sequence 3, Appl1
45	114	93.4	120	15	US-10-309-762-128	Sequence 128, App

ALIGNMENTS

RESULT 1
US-10-468-924-6
; Sequence 6, Application US/10468924
; Publication No. US20040127408A1
; GENERAL INFORMATION:
; APPLICANT: YEDA Research and Development Co. Ltd
; TITLE OF INVENTION: Synthetic Human Peptides and Pharmaceutical Compositions Compris
; FILE REFERENCE: TEVA-003 PCT
; CURRENT APPLICATION NUMBER: US/10/468,924
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: IL 141647
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Human
US-10-468-924-6

Query Match 100.0%; Score 122; DB 16; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWSWIRQPRGKEEWIG 19
|||
Db 1 GYWSWIRQPRGKEEWIG 19

RESULT 2
US-10-758-572-1
; Sequence 1, Application US/10758572
; Publication No. US20040180059A1
; GENERAL INFORMATION:

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OY      1 GYWWSWIRPPGKGEWIG 19  
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Db      1 GYWWSWIROPCKGEWIG 19
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RESULT 4
US-10-758-397-18
; Sequence 18, Application US/10758397
; Publication No. US2005008634A1
; GENERAL INFORMATION:
APPLICANT: Cohen-Vereid, et al., Sharon
TITLE OF INVENTION: PARENTERAL FORMULATIONS OF PEPTIDES FOR THE TREATMENT OF SYSTEMIC
FILE REFERENCE: 2609/68811-A
CURRENT APPLICATION NUMBER: US/10758,397
CURRENT FILING DATE: 2004-01-14
NUMBER OF SEQ ID NOS: 18

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Query Match          100.0%; Score 122; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches      19; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

Qy              1 GYYSWIRPPGKGEHWIG 19
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Db              2 GYYSWIRPPGKGEHWIG 20

RESULT 6
US-10-468-924-15
; Sequence 15, Application US/10468924
; Publication No. US20040127408A1
; GENERAL INFORMATION:
; APPLICANT: YEDA Research and Development Co. Ltd
; APPLICANT: MOZES, Edna
; TITLE OF INVENTION: Synthetic Human Peptides and Pharmaceutical Compositions Compris
; TITLE OF INVENTION: for the treatment of Systemic Lupus Erythematosus
; FILE REFERENCE: TEVA-003 PCT
; CURRENT APPLICATION NUMBER: US/10/468,924
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: IL 141647
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 19
; TYPE: PRP

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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: A peptide of SEQ ID NO: 11 wherein Xaa(1) is Gly, Xaa(8) is Lys,
OTHER INFORMATION: Xaa(10) is Pro, Xaa(12) is Gly, Xaa(13) is Lys, and Xaa(15) is Gl
US-10-468-924-15

Query Match 97.5%; Score 119; DB 16; Length 19;

Best Local Similarity 94.7%; Pred. No. 4.3e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWSWIRQPPKGSEWIG 19
Db 1 GYWSWIRQPPKGSEWIG 19

RESULT 7
US-10-468-924-13

Sequence 13, Application US/10468924
Publication No. US20040127408A1

GENERAL INFORMATION:

APPLICANT: YEDA Research and Development Co. Ltd
APPLICANT: MOZES, Edna

TITLE OF INVENTION: Synthetic Human Peptides and Pharmaceutical Compositions Comprisi
FILE REFERENCE: TEVA-003 PCT

CURRENT APPLICATION NUMBER: US/10/468,924

PRIOR FILING DATE: 2003-08-21

PRIOR APPLICATION NUMBER: IL 141647

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PatentIn version 3.1

SEQ ID NO 13

LENGTH: 19

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: A peptide of SEQ ID NO: 11 wherein Xaa(1) is Gly, Xaa(8) is Arg,
OTHER INFORMATION: Xaa(10) is Pro, Xaa(12) is Gly, Xaa(13) is Lys, and Xaa(15) is Se
US-10-468-924-13

Query Match 95.9%; Score 117; DB 16; Length 19;

Best Local Similarity 94.7%; Pred. No. 7.6e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYWSWIRQPPKGSEWIG 19
Db 1 GYWSWIRQPPKGSEWIG 19

RESULT 8
US-10-468-924-14

Sequence 14, Application US/10468924
Publication No. US20040127408A1

GENERAL INFORMATION:

APPLICANT: YEDA Research and Development Co. Ltd
APPLICANT: MOZES, Edna

TITLE OF INVENTION: Synthetic Human Peptides and Pharmaceutical Compositions Comprisi
FILE REFERENCE: TEVA-003 PCT

CURRENT APPLICATION NUMBER: US/10/468,924

PRIOR FILING DATE: 2003-08-21

PRIOR APPLICATION NUMBER: IL 141647

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PatentIn version 3.1

SEQ ID NO 14

LENGTH: 19

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: A peptide of SEQ ID NO: 11 wherein Xaa(1) is Gly, Xaa(8) is Arg,

OTHER INFORMATION: Xaa(10) is Pro, Xaa(12) is Gly, Xaa(13) is Asp, and Xaa(15) is C
OTHER INFORMATION: u.
US-10-468-924-14

Query Match 95.1%; Score 116; DB 16; Length 19;

Best Local Similarity 94.7%; Pred. No. 1e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYWSWIRQPPKGSEWIG 19
Db 1 GYWSWIRQPPKGSEWIG 19

RESULT 9
US-09-880-748-1326

Sequence 1326, Application US/09880748
Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PFS23

CURRENT APPLICATION NUMBER: US/09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1326

LENGTH: 252

TYPE: PRT

ORGANISM: Homo sapiens

US-09-880-748-1326

Query Match 95.1%; Score 116; DB 10; Length 252;

Best Local Similarity 94.7%; Pred. No. 1e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYWSWIRQPPKGSEWIG 19
Db 31 GYWSWIRQPPKGSEWIG 49

RESULT 10
US-10-293-418-1326

Sequence 1326, Application US/10293418
Publication No. US20030223996A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PFS23P2

CURRENT APPLICATION NUMBER: US/10/293,418

PRIOR FILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/240,816

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; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1326
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1326

Query Match          95.4%; Score 116; DB 15; Length 252;
Best Local Similarity 94.7%; Pred. No. 1e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19
   |||||
Db 31 GYWSWIRPPGKGEWIG 49

RESULT 11
US-10-468-924-12
; Sequence 12, Application US/10468924
; Publication No. US20040127408A1
; GENERAL INFORMATION:
; APPLICANT: YEDA Research and Development Co. Ltd
; APPLICANT: MOZES, Edna
; TITLE OF INVENTION: Synthetic Human Peptides and Pharmaceutical Compositions Comprisi
; FILE REFERENCE: TEVA-003 PCT
; CURRENT APPLICATION NUMBER: US/10/468,924
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: IL 141647
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A peptide of SEQ ID NO: 11 wherein Xaa(1) is Gly, Xaa(8) is Arg,
; OTHER INFORMATION: Xaa(10) is Pro, Xaa(12) is Gly, Xaa(13) is Lys, and Xaa(15) is Le
; OTHER INFORMATION: u.
US-10-468-924-12

Query Match          93.4%; Score 114; DB 16; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19
   |||||
Db 1 GYWSWIRPPGKGEWIG 19

RESULT 12
US-10-468-924-16
; Sequence 16, Application US/10468924
; Publication No. US20040127408A1
; GENERAL INFORMATION:
; APPLICANT: YEDA Research and Development Co. Ltd
; APPLICANT: MOZES, Edna
; TITLE OF INVENTION: Synthetic Human Peptides and Pharmaceutical Compositions Comprisi
; FILE REFERENCE: TEVA-003 PCT
; CURRENT APPLICATION NUMBER: US/10/468,924
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: IL 141647
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 19
; TYPE: PRT
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A peptide of SEQ ID NO: 11 wherein Xaa(1) is Gly, Xaa(8) is Arg,
; OTHER INFORMATION: Xaa(10) is Ser, Xaa(12) is Gly, Xaa(13) is Lys, and Xaa(15) is G
; OTHER INFORMATION: u.
US-10-468-924-16

Query Match          93.4%; Score 114; DB 16; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19
   |||||
Db 1 GYWSWIRPPGKGEWIG 19

RESULT 13
US-10-468-924-17
; Sequence 17, Application US/10468924
; Publication No. US20040127408A1
; GENERAL INFORMATION:
; APPLICANT: YEDA Research and Development Co. Ltd
; APPLICANT: MOZES, Edna
; TITLE OF INVENTION: Synthetic Human Peptides and Pharmaceutical Compositions Comprisi
; FILE REFERENCE: TEVA-003 PCT
; CURRENT APPLICATION NUMBER: US/10/468,924
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: IL 141647
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A peptide of SEQ ID NO: 11 wherein Xaa(1) is Gly, Xaa(8) is Arg,
; OTHER INFORMATION: Xaa(10) is Pro, Xaa(12) is Glu, Xaa(13) is Lys, and Xaa(15) is G
; OTHER INFORMATION: u.
US-10-468-924-17

Query Match          93.4%; Score 114; DB 16; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19
   |||||
Db 1 GYWSWIRPPGKGEWIG 19

RESULT 14
US-10-078-958-2
; Sequence 2, Application US/10078958
; Publication No. US20030070185A1
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AYA
; APPLICANT: KOCHERLAPATI, RAJU
; APPLICANT: KLAPHOLZ, SUSAN
; APPLICANT: MENDEZ, MICHAEL J.
; APPLICANT: GEEIN, LARRY
; TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN IG LOCI INCLUDING
; TITLE OF INVENTION: PLURAL VH AND VK REGIONS AND ANTIBODIES PRODUCED
; FILE REFERENCE: CELL 4.18 CON
; CURRENT APPLICATION NUMBER: US/10/078,958
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 08/759,620
; PRIOR FILING DATE: 1996-12-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 80
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TYPE: PRT
ORGANISM: Homo sapiens
US-10-078-958-2

Query Match 93.4%; Score 114; DB 14; Length 80;
Best Local Similarity 94.7%; Pred. No. 6.4e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYWSWIRQPPKGLEWIG 19
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Db 14 GYWSWIRQPPKGLEWIG 32

RESULT 15
US-10-194-975-40
; Sequence 40, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Roore, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-40

Query Match 93.4%; Score 114; DB 14; Length 97;
Best Local Similarity 94.7%; Pred. No. 7.6e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYWSWIRQPPKGLEWIG 19
|||
Db 31 GYWSWIRQPPKGLEWIG 49

Search completed: April 25, 2005, 16:18:45
Job time : 135 secs

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OM protein - protein search, using sw model

Run on: April 25, 2005, 15:56:43 ; Search time 39 Seconds
(without alignments)
46.875 Million cell updates/sec

Title: US-10-758-572-1

Perfect score: 122
Sequence: 1 GYWSWIRQPRKGEWIG 19

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 263416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 263416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR.79.*
2: PIR1.*
3: PIR2.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	117	95.9	143	2	B49028
2	114	93.4	97	2	S26898
3	114	93.4	97	2	S26806
4	114	93.4	97	2	S26805
5	114	93.4	97	2	S14474
6	114	93.4	106	2	S37454
7	114	93.4	122	2	UJ0047
8	114	93.4	126	2	S47010
9	114	93.4	140	2	S78052
10	114	93.4	140	2	A49045
11	111	91.0	146	1	G1HMH2
12	110	90.2	98	2	S26902
13	110	90.2	98	2	S12421
14	110	90.2	123	1	S30530
15	110	90.2	129	1	D2HUMA
16	110	90.2	140	2	A24770
17	109	89.3	137	2	S34149
18	108	88.5	39	2	S26937
19	108	88.5	97	2	S26906
20	108	88.5	97	2	G34964
21	108	88.5	97	2	S12416
22	108	88.5	99	2	S26802
23	108	88.5	99	2	S26803
24	108	88.5	105	2	S44125
25	108	88.5	114	2	I72667
26	108	88.5	116	2	B26340
27	108	88.5	118	2	A26340
28	108	88.5	140	2	I37782
29	108	88.5	146	2	S09711

30	108	88.5	155	2	S31512	Ig heavy chain - h
31	108	88.5	155	2	S31511	Ig heavy chain - h
32	108	88.5	231	2	B23746	Ig Fab region IV-J
33	105	86.1	97	2	PL0118	Ig heavy chain V-I
34	105	86.1	97	2	JH0428	Ig gamma chain V r
35	105	86.1	99	2	S26801	Ig heavy chain V r
36	105	86.1	99	2	S26807	Ig heavy chain V r
37	105	86.1	99	2	S26899	Ig heavy chain V r
38	105	86.1	116	2	S37456	Ig mu chain - huma
39	104	85.2	39	2	S26939	Ig heavy chain V r
40	104	85.2	99	2	S26800	Ig heavy chain V r
41	104	85.2	99	2	S12412	Ig heavy chain V r
42	104	85.2	99	2	S12418	Ig heavy chain V r
43	104	85.2	100	2	S78056	Ig heavy chain V r
44	104	85.2	110	2	S44110	Ig heavy chain V-D
45	104	85.2	124	2	S31684	Ig heavy chain V r

ALIGNMENTS

RESULT 1
B49028
Ig heavy chain V-IV region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C:Accession: B49028
R:Zimmers, E.; Kentler, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schu
Bur, J. Immunol. 21, 2355-2363, 1991
A:Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lympho
A:Reference number: A49028; MUID:92008140; PMID:1915549
A:Accession: B49028
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-143 <TIM>
A:Cross-references: GB:S64473; NID:G236906; PIDN:AB20012.1; PID:G236907
A:Experimental source: X-linked agammaglobulinemia patients, B lymphoblastoid cell line
A>Note: Sequence extracted from NCI backbone (NCBI:64473, NCBI:64472)
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 95.9%; Score 117; DB 2; Length 143;
Best Local Similarity 94.7%; Pred. No. 1.2e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYWSWIRQPRKGEWIG 19
DB 31 GYWSWIRQPRKGEWIG 49

RESULT 2
S26898
Ig heavy chain V region (clone DP-63, V(H)4.2) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26898; S12420
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26898
A:Molecule type: DNA
A:Residues: 1-97 <TOM>
A:Cross-references: EMBL:Z1363; NID:G32944; PIDN:CA78233.1; PID:G32945
A:Experimental source: Clone DP-63
R:Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A:Title: The smaller human V(H) gene families display remarkably little polymorphism.
A:Reference number: S09421; MUID:90059975; PMID:2511001
A:Accession: S12420
A:Status: translation not shown
A:Molecule type: DNA

A;Residues: 1-97 <SANT>

A;Cross-references: EMBL:X56364

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C;Accession: S26806

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-97//Domain: immunoglobulin homology <IMM>

Query Match 93.4%; Score 114; DB 2; Length 97;

Best Local Similarity 94.7%; Pred. No. 2.1e-08; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19

DB 31 GYWSWIRPPGKGEWIG 49

RESULT 3

S26806

Ig heavy chain V region - human

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C;Accession: S26806

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-97//Domain: immunoglobulin homology <IMM>

A;Residues: 1-97 <WEN>

A;Cross-references: EMBL:X56364; NID:G37716; PIDN:CA47861.1; PID:G1335377

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-97//Domain: immunoglobulin homology <IMM>

Query Match 93.4%; Score 114; DB 2; Length 97;

Best Local Similarity 94.7%; Pred. No. 2.1e-08; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19

DB 31 GYWSWIRPPGKGEWIG 49

RESULT 4

S26805

Ig heavy chain V region - human

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C;Accession: S26805

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-97//Domain: immunoglobulin homology <IMM>

A;Residues: 1-97 <WEN>

A;Cross-references: EMBL:X56364; NID:G37714; PIDN:CA47861.1; PID:G1335376

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-97//Domain: immunoglobulin homology <IMM>

Query Match 93.4%; Score 114; DB 2; Length 97;

Best Local Similarity 94.7%; Pred. No. 2.1e-08; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19

DB 31 GYWSWIRPPGKGEWIG 49

RESULT 5

S14474

Ig heavy chain V region - human

C;Species: Homo sapiens (man)

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000

C;Accession: S14474

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-97//Domain: immunoglobulin homology <IMM>

Query Match 93.4%; Score 114; DB 2; Length 97;

Best Local Similarity 94.7%; Pred. No. 2.1e-08; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19

DB 31 GYWSWIRPPGKGEWIG 49

RESULT 6

S37454

Ig mu chain - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C;Accession: S37454

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-97//Domain: immunoglobulin homology <IMM>

A;Residues: 1-106 <MCI>

A;Cross-references: EMBL:X5022; NID:G404311; PIDN:CA45230.1; PID:G758093

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-97//Domain: immunoglobulin homology <IMM>

Query Match 93.4%; Score 114; DB 2; Length 106;

Best Local Similarity 94.7%; Pred. No. 2.3e-08; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19

DB 9 GYWSWIRPPGKGEWIG 27

RESULT 7

JL0047

Ig heavy chain V region precursor (clone cR18) - human

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996

C;Accession: JL0047

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-97//Domain: immunoglobulin homology <IMM>

A;Residues: 1-122 <BAE>

A;Cross-references: EMBL:X56364; NID:G37714; PIDN:CA47861.1; PID:G1335376

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-97//Domain: immunoglobulin homology <IMM>

Query Match 93.4%; Score 114; DB 2; Length 106;

Best Local Similarity 94.7%; Pred. No. 2.3e-08; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19

DB 9 GYWSWIRPPGKGEWIG 27

RESULT 8

JL0047

Ig heavy chain V region precursor (clone cR18) - human

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996

C;Accession: JL0047

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-97//Domain: immunoglobulin homology <IMM>

Query Match 93.4%; Score 114; DB 2; Length 106;

Best Local Similarity 94.7%; Pred. No. 2.3e-08; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19

DB 9 GYWSWIRPPGKGEWIG 27

Query Match 93.4%; Score 114; DB 2; Length 122;
Best Local Similarity 94.7%; Pred. No. 2.7e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRQPPGKGEWIG 19
Db 39 GYWSWIRQPPGKGEWIG 57

RESULT 8

S47010
Ig heavy chain V4.21-UniqueD-J5 region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S47010
R:Maumond, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.
A:Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody birt
A:Reference number: S47009
A:Accession: S47010
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-126 <MAH>
A:Cross-references: EMBL:Z5492; NID:G517254; PIDN:CA64625.1; PID:G517255
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:13-97/Domain: immunoglobulin homology <IMM>

Query Match 93.4%; Score 114; DB 2; Length 126;
Best Local Similarity 94.7%; Pred. No. 2.7e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRQPPGKGEWIG 19
Db 31 GYWSWIRQPPGKGEWIG 49

RESULT 9

S78052
Ig heavy chain precursor V-D-J region (clone mAb 63VH) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C:Accession: S78052; S23717
R:Harindranath, N.
A:Submitted to the EMBL Data Library, August 1990
A:Reference number: S78051
A:Accession: S78052
A:Molecule type: mRNA
A:Residues: 1-140 <HAR>
A:Cross-references: EMBL:X54441; NID:G37815; PIDN:CA3308.1; PID:G930118
R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burratello, S.E.; Wilder, R.L.; Norkling
Int. Immunol. 3, 865-875, 1991
A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and H
patient.
A:Reference number: S23716; MUID:92031262; PMID:1718404
A:Accession: S23717
A:Molecule type: mRNA
A:Residues: 15-111 <HAM>
A:Cross-references: EMBL:X54441
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-14/Domain: signal sequence (fragment) #status predicted <SIG>
F:15-140/Product: Ig heavy chain (fragment) #status predicted <MAT>
F:29-111/Domain: immunoglobulin homology <IMM>

Query Match 93.4%; Score 114; DB 2; Length 140;
Best Local Similarity 94.7%; Pred. No. 3.1e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRQPPGKGEWIG 19
Db 45 GYWSWIRQPPGKGEWIG 63

RESULT 10
A49045
Ig heavy chain V region (anti-B cell autoantibody) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C:Accession: A49045
R:Grillot-Courvalin, C.; Brunet, J.C.; Piller, F.; Rasenti, L.Z.; Labaune, S.; Silvert
Eur. J. Immunol. 22, 1781-1788, 1992
A:Title: An anti-B cell autoantibody from Miskott-Aldrich syndrome which recognizes I t
A:Reference number: A49045; MUID:92324290; PMID:1623923
A:Accession: A49045
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140 <GRI>
A:Cross-references: GB:S39381; NID:G250899; PIDN:AMB22441.1; PID:G250900
A>Note: sequence extracted from NCBI backbone (NCBIN:108088, NCBIIP:108089)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 93.4%; Score 114; DB 2; Length 140;
Best Local Similarity 94.7%; Pred. No. 3.1e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRQPPGKGEWIG 19
Db 50 GYWSWIRQPPGKGEWIG 68

RESULT 11

G1HUH2
Ig heavy chain precursor V-II region (ARH-77) - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C:Accession: A02101
R:Kudo, A.; Ishihara, T.; Nishimura, Y.; Watanabe, T.
Gene 33, 181-189, 1985
A:Title: A cloned human immunoglobulin heavy chain gene with a novel direct-repeat sequ
A:Reference number: A02101; MUID:85205332; PMID:3922855
A:Accession: A02101
A:Molecule type: mRNA
A:Residues: 1-146 <KUD>
A:Cross-references: UNIPROT:P06331
A>Note: the sequence was determined from the differentiated gene
A>Note: the authors translated the codon GCG for residue 17 as Arg
C:Genetics:
A:Gene: GDB:IGHV@
A:Cross-references: GDB:128528; OMIM:147070
A:Map position: 14q32.33-14q32.33
A:Inserts: 16/3
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-146/Product: Ig heavy chain V-II region (ARH-77) #status predicted <MAT>
F:120-117/Region: V segment
F:35-117/Domain: immunoglobulin homology <IMM>
F:118-127/Region: D segment
F:128-146/Region: J segment
F:42-115/Distalide bonds: #status predicted

Query Match 91.0%; Score 111; DB 1; Length 146;
Best Local Similarity 89.5%; Pred. No. 8e-08;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRQPPGKGEWIG 19
Db 51 GYWSWIRQPPGKGEWIG 69

RESULT 12

S26902
Ig heavy chain V region (DP-67) - human (fragment)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 15:48:23 ; Search time 176 Seconds

(without alignments)
55.281 Million cell updates/sec

Title: US-10-758-572-1

Perfect score: 122
Sequence: 1 GYWSWIRQPPGKGEWIG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	93.4	595	2	Q6WUX4
2	114	93.4	597	2	Q6GMX5
3	114	93.4	597	2	Q6BQ88
4	114	93.4	597	2	Q9BU10
5	114	93.4	625	2	Q96AA6
6	111	91.0	116	2	Q7Z3Y6
7	111	91.0	146	1	HV2I_HUMAN
8	110	90.2	129	1	HV2F_HUMAN
9	108	88.5	119	2	Q9UL73
10	108	88.5	139	2	Q68SX2
11	108	88.5	476	2	Q6GMX1
12	106	86.9	465	2	Q6GMX6
13	104	85.2	492	2	Q7Z374
14	103	84.4	473	2	Q6TC63
15	100	82.0	620	2	Q96EY0
16	98	80.3	496	2	Q96KX8
17	96	78.7	130	2	Q81ZD7
18	96	78.7	150	2	Q95973
19	95	77.9	576	2	Q6P4I8
20	93	76.2	476	2	Q6MZK7
21	92	75.4	477	2	Q6GMX7
22	90	73.8	478	2	Q7Z379
23	88	72.1	98	2	Q6B6Z0
24	88	72.1	100	2	Q6B6Z2
25	88	72.1	117	1	HV4I_MOUSE
26	87	71.3	102	2	Q6B6S8
27	87	71.3	117	1	HV17_MOUSE
28	86	70.5	135	1	HV02_XENLA
29	85	69.7	117	1	HV2G_HUMAN
30	84	68.9	115	1	HV44_MOUSE
31	84	68.9	116	1	HV60_MOUSE

32	84	68.9	119	2	Q9GYZ2	Q9GYZ2 schistosoma
33	84	68.9	144	1	HV43_MOUSE	P01819 mus musculus
34	84	68.9	225	2	Q6PAF5	Q6PAF5 xenopus lae
35	84	68.9	479	2	Q99M22	Q99M22 mus musculus
36	84	68.9	484	2	Q8VEA0	Q8VEA0 mus musculus
37	83	68.0	117	1	HV2B_RABIT	P01828 oryctolagus
38	83	68.0	118	1	HV39_MOUSE	P01809 mus musculus
39	82	67.2	99	2	Q6B6T4	Q6B6T4 oryctolagus
40	82	67.2	101	2	Q6B6W2	Q6B6W2 oryctolagus
41	82	67.2	105	2	Q6B715	Q6B715 oryctolagus
42	82	67.2	116	1	HV36_MOUSE	P01806 mus musculus
43	82	67.2	117	1	HV42_MOUSE	P01812 mus musculus
44	82	67.2	119	1	HV37_MOUSE	P01807 mus musculus
45	82	67.2	119	1	HV38_MOUSE	P01808 mus musculus

ALIGNMENTS

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RESULT 1
ID Q6WUX4 PRELIMINARY; PRT; 595 AA.
AC Q6WUX4;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
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RN SEQUENCE FROM N.A.
RP TISSUE=Lymph;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Cavarni P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gamaralle P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywnicki M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Lymph;
RC Strausberg R.L.;
RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL, BC019235; AA019235.2; -.
DR PIR, G34964; G34964.
DR HSSP, P01861; IADQ.
DR Pfam, PF07654; CI-set; 4.
DR SMART, SM00409; IG, 2.
DR SMART, SM00407; IGL, 4.
DR SMART, SM00406; IGV, 1.
DR PROSITE, PS50835; IG LIKE; 5.
DR PROSITE, PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SEQUENCE 595 AA; 65290 MW; 0D4B5076545714E CRC64;
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Query Match 93.4%; Score 114; DB 2; Length 595;

Best Local Similarity 94.7%; Pred. No. 2.4e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIROPKGEWIG 19
Db 57 GYWSWIROPKGEWIG 75

RESULT 2

Q6GMX5 PRELIMINARY; PRT; 597 AA.
ID Q6GMX5
AC Q6GMX5
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph.
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haile F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph.
RA Strausberg R.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073767; AAH73767.1; -
DR InterPro; IPR003599; IG -
DR InterPro; IPR007110; IG -like.
DR InterPro; IPR003597; IG -cl.
DR InterPro; IPR003596; IG -MHC.
DR InterPro; IPR003596; IG -v.
DR Pfam; PF07654; Cl-sec; 4.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PSS0835; IG LIKE; 5.
DR PROSITE; PSS0290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65304 MW; 2A1E75FAED65230 CRC64;

Query Match 93.4%; Score 114; DB 2; Length 597;
Best Local Similarity 94.7%; Pred. No. 2.4e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIROPKGEWIG 19
Db 50 GYWSWIROPKGEWIG 68

RESULT 3

Q9B0B8 PRELIMINARY; PRT; 597 AA.
ID Q9B0B8
AC Q9B0B8
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haile F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.,
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006180; AAH06180.1; -
DR HSSP; P01861; IADO.
DR InterPro; IPR007110; IG -like.
DR InterPro; IPR003597; IG -cl.
DR InterPro; IPR003596; IG -MHC.
DR InterPro; IPR003596; IG -v.
DR Pfam; PF07654; Cl-sec; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PSS0835; IG LIKE; 5.
DR PROSITE; PSS0290; IG_MHC; UNKNOWN_3.
SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match 93.4%; Score 114; DB 2; Length 597;
Best Local Similarity 94.7%; Pred. No. 2.4e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIROPKGEWIG 19
Db 50 GYWSWIROPKGEWIG 68

RESULT 4

Q9B0B8 PRELIMINARY; PRT; 597 AA.
ID Q9B0B8
AC Q9B0B8
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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 Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RX Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RA EMBL, BC002963; AAH02963.1; -.
 DR HSP, P01861; IADQ.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003597; IG_C1.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF07654; C1-sect; 4.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG_LIKE; 5.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
 SQ SEQUENCE 597 AA; 65274 MW; 2DAF8B7E055851 CRC64;
 Query Match 93.4%; Score 114; DB 2; Length 597;
 Best Local Similarity 94.7%; Pred. No. 2.4e-07;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GYWSWIRPPKGEWIG 19
 DB 50 GYWSWIRPPKGEWIG 68
 RESULT 5
 ID 096AAG PRELIMINARY; PRT; 625 AA.
 AC 096AAG;
 DT 01-DEC-2001 (TREMBlrel. 19; Created)
 DT 01-DEC-2001 (TREMBlrel. 19; Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26; Last annotation update)
 DE IGHM protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
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 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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 Datchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
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 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RX Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 RA EMBL, BC017356; AAH17356.2; -.
 DR PIR: S15590; S15590.
 DR HSP, P01861; IADQ.
 DR InterPro: IPR003599; IG_1like.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003597; IG_C1.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF07654; C1-sect; 4.
 DR SMART: SM00409; IG; 2.
 DR SMART: SM00407; IGV; 4.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG_LIKE; 5.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
 SQ SEQUENCE 625 AA; 68610 MW; F62FAB3ADE7ECBE CRC64;
 Query Match 93.4%; Score 114; DB 2; Length 625;
 Best Local Similarity 94.7%; Pred. No. 2.5e-07;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GYWSWIRPPKGEWIG 19
 DB 57 GYWSWIRPPKGEWIG 75
 RESULT 6
 ID 0723Y6 PRELIMINARY; PRT; 116 AA.
 AC 0723Y6;
 DT 01-OCT-2003 (TREMBlrel. 25; Created)
 DT 01-OCT-2003 (TREMBlrel. 25; Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26; Last annotation update)
 DE Rearranged VH4-34 V gene segment (Fragment).
 GN Name=VH4-34;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hodgkin lymphoma;
 RA Tinguely M., Rosenquist R., Sundtrem C., Amini R.M., Kuipers R.,
 Hansmann M.L., Branninger A.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AJ564425; CAD92032.1; -.
 DR HSP, P18532; IKCV.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003596; IG_V.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG_LIKE; 1.
 FT NON TER 1 1
 FT NON TER 116 116
 SQ SEQUENCE 116 AA; 12902 MW; CE3DBA846616C908 CRC64;

RA Stadelton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 Rana S.S., Loquellano N.A., Peters G.J., Abrahamson R.D., Mullany S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RX Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 RA EMBL, BC017356; AAH17356.2; -.
 DR PIR: S15590; S15590.
 DR HSP, P01861; IADQ.
 DR InterPro: IPR003599; IG_1like.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003597; IG_C1.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF07654; C1-sect; 4.
 DR SMART: SM00409; IG; 2.
 DR SMART: SM00407; IGV; 4.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG_LIKE; 5.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
 SQ SEQUENCE 625 AA; 68610 MW; F62FAB3ADE7ECBE CRC64;
 Query Match 93.4%; Score 114; DB 2; Length 625;
 Best Local Similarity 94.7%; Pred. No. 2.5e-07;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GYWSWIRPPKGEWIG 19
 DB 57 GYWSWIRPPKGEWIG 75
 RESULT 6
 ID 0723Y6 PRELIMINARY; PRT; 116 AA.
 AC 0723Y6;
 DT 01-OCT-2003 (TREMBlrel. 25; Created)
 DT 01-OCT-2003 (TREMBlrel. 25; Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26; Last annotation update)
 DE Rearranged VH4-34 V gene segment (Fragment).
 GN Name=VH4-34;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hodgkin lymphoma;
 RA Tinguely M., Rosenquist R., Sundtrem C., Amini R.M., Kuipers R.,
 Hansmann M.L., Branninger A.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AJ564425; CAD92032.1; -.
 DR HSP, P18532; IKCV.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003596; IG_V.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG_LIKE; 1.
 FT NON TER 1 1
 FT NON TER 116 116
 SQ SEQUENCE 116 AA; 12902 MW; CE3DBA846616C908 CRC64;

Query Match 91.0%; Score 111; DB 2; Length 116;
Best Local Similarity 89.5%; Pred. No. 1.3e-07;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYWSWIRPPGKGEWIG 19
Db 31 GYWSWIRPPGKGEWIG 49

RESULT 7
ID HUMAN STANDARD; PRT; 146 AA.
AC P01824;
DT 01-JUN-1988 (Rel. 06, Created)
DT 01-JUN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region ARH-77 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=85205332; PubMed=3922855; DOI=10.1016/0378-1119(85)90092-7;
RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
RT "A cloned human immunoglobulin heavy chain gene with a novel direct-
repeat sequence in 5' flanking region.";
RL Gene 33:181-189(1985).
RL PIR; A02101; GIHMH2.
DR HSSP; P01825; 7PAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PSS0835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.

FT CHAIN 1 19 Ig heavy chain V-II region ARH-77.
FT DOMAIN 20 146 V segment.
FT DOMAIN 118 127 D segment.
FT DOMAIN 128 146 U segment.
FT DISULFID 42 115 By similarity.
FT NON_TER 146 146
SQ SEQUENCE 146 AA; 16228 MW; 807PD52BB218171F CRC64;

Query Match 91.0%; Score 111; DB 1; Length 146;
Best Local Similarity 89.5%; Pred. No. 1.6e-07;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYWSWIRPPGKGEWIG 19
Db 51 GYWSWIRPPGKGEWIG 69

RESULT 8
ID HUMAN STANDARD; PRT; 129 AA.
AC P01824;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-II region WAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=82222235; PubMed=6806818;

RA Takahashi N., Tetaert D., Debure B., Lin L.-C., Putnam F.W.;
RT "Complete amino acid sequence of the delta heavy chain of human
immunoglobulin D.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
CC -1- MISCELLANEOUS: This chain was isolated from an Igd myeloma
protein.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02099; D2HUMA.
DR HSSP; P01820; 1G7J.
DR Glycosylated; P01824; -.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PSS0835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 113
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE5119 CRC64;

Query Match 90.2%; Score 110; DB 1; Length 129;
Best Local Similarity 89.5%; Pred. No. 1.9e-07;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYWSWIRPPGKGEWIG 19
Db 33 GYWSWIRPPGKGEWIG 51

RESULT 9
ID GUL73 PRELIMINARY; PRT; 119 AA.
AC Q9UL73;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9827139; PubMed=9614934; DOI=10.1006/cclin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
feetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RL EMBL; AF035041; AAD56277.1; -.
DR PIR; PH0876; PH0876.
DR PIR; S12416; S12416.
DR HSSP; P01820; 1G7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PSS0835; IG LIKE; 1.
FT NON_TER 1 119
SQ SEQUENCE 119 AA; 13219 MW; 1BD86B6420EAOBE CRC64;

Query Match 88.5%; Score 108; DB 2; Length 119;
Best Local Similarity 94.4%; Pred. No. 3.3e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YWSWIRPPGKGEWIG 19
Db 32 YWSWIRPPGKGEWIG 49

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RESULT 10
O66SX2      PRELIMINARY;      PRT;      139 AA.
AC O66SX2;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Full-length cDNA clone CS0DL004YM19 of B cells (Ramos cell line) of
DE Homo sapiens (human).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Li W.B., Gruber C., Jessee J., Polayes D.;
RL Submitted (FEB-2003) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Genoscope;
RL Submitted (FEB-2003) to the EMBL/Genbank/DBJ databases.
DR HSSP; P01820; 1G7J
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON TER
SQ SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;

Query Match      88.5%; Score 108; DB 2; Length 139;
Best Local Similarity 94.4%; Pred. No. 3.9e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 YWMSIROPKGEWIG 19
Db 64 YWMSIROPKGEWIG 81

RESULT 11
O6GMX1      PRELIMINARY;      PRT;      476 AA.
AC O6GMX1;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

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RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strauberg R.;
RL Submitted (JUN-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC073773; AAH73773.1; -
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-sect; 3.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AAB5C62DDE9D CRC64;

Query Match      88.5%; Score 108; DB 2; Length 476;
Best Local Similarity 94.4%; Pred. No. 1.3e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 YWMSIROPKGEWIG 19
Db 53 YWMSIROPKGEWIG 70

RESULT 12
O6GMX6      PRELIMINARY;      PRT;      465 AA.
AC O6GMX6;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.

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RC TISSUE=Primary B-cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PSS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match 86.9%; Score 106; DB 2; Length 465;
Best Local Similarity 89.5%; Pred. No. 2.4e-06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 GYWSWIRPPGKGEWIG 19
50 GYWSWIRPPGKGEWIG 68

RESULT 13
ID Q72374 PRELIMINARY; PRT; 492 AA.
AC Q72374;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZ686C02218 (Fragment).
GN Name=DKFZ686C02218;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Fodor G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX38077; CAD98001.1; -.
DR HSSP; P01820; 1G7J.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00406; IG; 1.
DR PROSITE; PSS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR Hypothetical protein.
KM NON TER 1
SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;

Query Match 85.2%; Score 104; DB 2; Length 492;
Best Local Similarity 88.9%; Pred. No. 4.8e-06;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 2 YWSMIROPKGEWIG 19
65 YWSMIROPKGEWIG 82

RESULT 14
ID Q8TC63 PRELIMINARY; PRT; 473 AA.
Q8TC63
Q8TC63

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AC Q8TC63;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHG4 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; Pubmed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schlier G.D.,
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.L., Wang J., Hsien F.,
RA Diachenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Tohilyuki S., Carninci P., Mullahy S.J.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skala U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025985; AAH25985.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00196; COPPER BLUE; UNKNOWN_1.
DR PROSITE; PSS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 84.4%; Score 103; DB 2; Length 473;
Best Local Similarity 83.3%; Pred. No. 6.3e-06;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 2 YWSMIROPKGEWIG 19
60 YWSMIROPKGEWIG 77

RESULT 15
ID Q96EY0 PRELIMINARY; PRT; 620 AA.
AC Q96EY0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;

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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Ditschenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.U., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strauberg R.;
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC011857; AAH1857.2; -.
DR PIR; S15590; S15590.
DR HSP; P01820; I67J.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG-MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-bee; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 620 AA; 68125 MW; 990A1A4A6E8FF27B CRC64;

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Query Match 82.0%; Score 100; DB 2; Length 620;
 Best local Similarity 88.9%; Pred. No. 2.1e-05;
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QY 2 YYMSWIRPPKSGEWTG 19
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DB 58 YYMSWIRPPKSGEWTG 75

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